

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lee, Se-Jin
Huynh, Thanh
- (ii) TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/581,529
 - (B) FILING DATE: 15-APR-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lisa A. Haile, Ph.D.
 - (B) REGISTRATION NUMBER: 38,347
 - (C) REFERENCE/DOCKET NUMBER: 07265/082001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 678-5070
 - (B) TELEFAX: (619) 678-5099

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: SJL141

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..35
 - (D) OTHER INFORMATION: /note= "V=guanine, cytosine or adenine; N=adenine, cytosine, guanine or thymine; R=adenine or guanine; Y=cytosine or thymine; K=thymine or guanine; N=inosine"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGAATTTCG GNTGGVANRA YTGGRNRTN KCNCC

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:

(B) CLONE: SJL145

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..29
- (C) OTHER INFORMATION: /note= "R=adenine or guanine;
S=cytosine or guanine; M=adenine or cytosine;
N=adenine, cytosine, guanine or thymine;
Y=cytosine or thymine; N=inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

33

CCGGAATTCTC CANSCRCANG MNTCNACNRY CAT

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: SJL141

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /note= "Xaa at position 3=His, Gln,
Asn, Lys, Asp or Glu; Xaa at position 4=Asp or
Asn; Xaa at positions 6 and 7=Val, Ile or Met;
Xaa at position 8=Ala or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Trp Xaa Xaa Trp Xaa Xaa Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: SJL145

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..8
- (D) OTHER INFORMATION: /note= "Xaa at position 2=Val,
Ile, Met, Thr or Ala; Xaa at position 4=Asp or Glu;
Xaa at position 5=Ala or Ser; Xaa at position 6=Gly
or Ala"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Xaa Val Xaa Xaa Cys Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
(3) CLONE: GDF-6

(ix) FEATURE:
(A) NAME/KEY: CDS
(3) LOCATION: 126..527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCCCTGCTTG TAGTGTTCAC CAGATCGCAG CGCAAGAACC TGTTCACTGA GATGCATGAG	60
CAGCTGGGCT CTGCAGAGGC TGCGGGAGCC GAGGGGTCAT GGCCAGCGCC GTCGGGCTCC	120
CAGAC GCC GGG TCT TGG CTG CCC TCG CCC GGC CGC CGG CGA CGC	167
Ala Gly Ser Trp Leu Pro Ser Pro Gly Arg Arg Arg Arg Arg	
1 5 10	
ACC GCC TTC GCC AGC CGT CAC GGC AAG CGA CAT GGC AAG AAG TCC AGG	215
Thr Ala Phe Ala Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg	
15 20 25 30	
CTG CGC TGC AGC AGA AAG CCT CTG CAC GTG AAT TTT AAG GAG TTA GGC	263
Leu Arg Cys Ser Arg Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly	
35 40 45	
TGG GAC GAC TGG ATT ATC GCG CCC CTA GAG TAC GAG GCC TAT CAC TGC	311
Trp Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys	
50 55 60	
GAG GGC GTG TGC GAC TTT CCG CTG CGC TCG CAC CTT GAG CCC ACT AAC	359
Glu Gly Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn	
65 70 75	
CAT GCC ATC ATT CAG ACG CTG ATG AAC TCC ATG GAC CCG GGC TCC ACC	407
His Ala Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr	
80 85 90	
CCG CCT AGC TGC TGC GTT CCC ACC AAA CTG ACT CCC ATT AGC ATC CTG	455
Pro Pro Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu	
95 100 105 110	
TAC ATC GAC GGC GGC AAT AAT GTA GTC TAC AAG CAG TAT GAG GAC ATG	503
Tyr Ile Asp Ala Gly Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met	
115 120 125	
GTG GTG GAG TCC TGC GGC TGT AGG TAG	530
Val Val Glu Ser Cys Gly Cys Arg	
130	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Gly Ser Trp Leu Pro Ser Pro Gly Arg Arg Arg Arg Thr Ala	15
1 5 10	
Phe Ala Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu Arg	30
20 25 30	
Cys Ser Arg Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp	45
35 40 45	
Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly	60
50 55 60	
Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala	80
65 70 75 80	
Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro	95
85 90 95	

Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile
 100 105 110
 Asp Ala Gly Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val
 115 120 125
 Glu Ser Cys Gly Cys Arg
 130

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
 (B) CLONE: GDF-6 (C-terminal)

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Phe Ala Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu
 1 5 10 15
 Arg Cys Ser Arg Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp
 20 25 30
 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu
 35 40 45
 Gly Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
 50 55 60
 Ala Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro
 65 70 75 80
 Pro Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr
 85 90 95
 Ile Asp Ala Gly Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
 100 105 110
 Val Glu Ser Cys Gly Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
 (B) CLONE: GDF-1

(ix) FEATURE:

(A) NAME/KEY: Protein
(B) LOCATION: 1..123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly
1 5 10 15
Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp
20 25 30
His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln
35 40 45
Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro
50 55 60
Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro
65 70 75 80
Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile
85 90 95
Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr
100 105 110
Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
115 120

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: BMP-2

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser
1 5 10 15
Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
20 25 30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His
35 40 45
Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
50 55 60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys
65 70 75 80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
85 90 95

Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val
 100 105 110

Glu Gly Cys Gly Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
 (B) CLONE: BMP-4

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys
 1 5 10 15
 Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
 20 25 30
 Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His
 35 40 45
 Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
 50 55 60
 Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys
 65 70 75 80
 Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
 85 90 95
 Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val
 100 105 110
 Glu Gly Cys Gly Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
 (B) CLONE: Vgr-1

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Arg Gly Ser Gly Ser Ser Asp Tyr Asn Gly Ser Glu Leu Lys Thr
1 5 10 15
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp
20 25 30
Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp
35 40 45
Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
50 55 60
Ala Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro
65 70 75 80
Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr
85 90 95
Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
100 105 110
Val Arg Ala Cys Gly Cys His
115

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: OP-1

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln
1 5 10 15
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp
20 25 30
Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu
35 40 45
Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His
50 55 60
Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro
65 70 75 80
Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr
85 90 95
Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
100 105 110

Val Arg Ala Cys Gly Cys His
115

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: BMP-5

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ser Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln
1 5 10 15
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp
20 25 30
Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp
35 40 45
Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
50 55 60
Ala Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro
65 70 75 80
Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr
85 90 95
Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
100 105 110
Val Arg Ser Cys Gly Cys His
115

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: BMP-3

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg
1 5 10 15

Asn Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp
 20 25 30

Ser Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser
 35 40 45

Gly Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His
 50 55 60

Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile
 65 70 75 80

Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
 85 90 95

Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
 100 105 110

Thr Val Glu Ser Cys Ala Cys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: MIS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Pro Gly Arg Ala Gln Arg Ser Ala Gly Ala Thr Ala Ala Asp Gly
 1 5 10 15

Pro Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser
 20 25 30

Val Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Val Cys
 35 40 45

Gly Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val
 50 55 60

Leu Leu Leu Lys Met Gln Ala Arg Gly Ala Ala Leu Ala Arg Pro Pro
 65 70 75 80

Cys Cys Val Pro Thr Ala Tyr Ala Gly Lys Leu Leu Ile Ser Leu Ser
 85 90 95

Glu Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu
 100 105 110

Cys Gly Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibin-alpha

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro Ala Ala His Ala
1 5 10 15

Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp
20 25 30

Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His
35 40 45

Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro
50 55 60

Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala
65 70 75 80

Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val
85 90 95

Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro
100 105 110

Asn Leu Leu Thr Gln His Cys Ala Cys Ile
115 120

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibin-beta-alpha

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile
1 5 10 15

Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
 20 25 30
 Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
 35 40 45
 Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
 50 55 60
 His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
 65 70 75 80
 Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
 85 90 95
 Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
 100 105 110
 Asn Met Ile Val Glu Glu Cys Gly Cys Ser
 115 120

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Inhibin-beta-beta

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His Arg Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu
 1 5 10 15
 Cys Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn
 20 25 30
 Asp Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly
 35 40 45
 Ser Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe
 50 55 60
 His Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly
 65 70 75 80
 Thr Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met
 85 90 95
 Leu Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn
 100 105 110
 Met Ile Val Glu Glu Cys Gly Cys Ala
 115 120

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(S) CLONE: TGF-beta-1

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
1 5 10 15

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 20 25 30

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 35 40 45

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 50 55 60

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
65 70 75 80

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 85 90 95

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 100 105 110

Lys Cys Ser
 115

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: TGF-beta-2

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Lys Arg Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp
1 5 10 15

Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly
 20 25 30
 Trp Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala
 35 40 45
 Gly Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val
 50 55 60
 Leu Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys
 65 70 75 80
 Cys Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly
 85 90 95
 Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys
 100 105 110
 Lys Cys Ser
 115

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
 (B) CLONE: TGF-beta-3

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Lys Arg Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu
 1 5 10 15
 Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly
 20 25 30
 Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser
 35 40 45
 Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val
 50 55 60
 Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys
 65 70 75 80
 Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly
 85 90 95
 Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys
 100 105 110
 Lys Cys Ser
 115